

# SEQUENCE LISTING

<110> Osteryoung, Katherine W.

<120> Manipulation of Min Genes in Plants

<130> 920905.90041

5 <140>

<141>

<150> 60/130,403

<151> 1999-04-19

<160> 4

10 <170> PatentIn Ver. 2.1

<210> 1

<211> 978

<212> DNA

<213> Arabidopsis thaliana

15 <220>

<221> CDS

<222> (1)..(978)

<400> 1

20	atg gcg tct ctg aga ttg ttc tca acg aat cat caa tct ctt ctc ctt	48
	Met Ala Ser Leu Arg Leu Phe Ser Thr Asn His Gln Ser Leu Leu Leu	
	1 5 10 15	
	cca tca tct ctc tca caa aag act cta ata tct tca cca aga ttc gtc	96
	Pro Ser Ser Leu Ser Gln Lys Thr Leu Ile Ser Ser Pro Arg Phe Val	
	20 25 30	
25	aat aac cct agc aga cgg agt cca ata cga tcc gtt ctt caa ttt aat	144
	Asn Asn Pro Ser Arg Arg Ser Pro Ile Arg Ser Val Leu Gln Phe Asn	
	35 40 45	
30	cgc aaa ccg gaa ctc gcc gga gaa acg ccg cgt atc gtc gtt atc acc	192
	Arg Lys Pro Glu Leu Ala Gly Glu Thr Pro Arg Ile Val Val Ile Thr	
	50 55 60	
	tcc gga aaa ggc ggt gtt gga aag acg aca acc acc gca aat gtc ggt	240
	Ser Gly Lys Gly Gly Val Gly Lys Thr Thr Thr Thr Ala Asn Val Gly	
	65 70 75 80	
35	ctc tct ctc gct cgt tac ggt ttc tca gtt gtc gcc att gac gcc gac	288
	Leu Ser Leu Ala Arg Tyr Gly Phe Ser Val Val Ala Ile Asp Ala Asp	
	85 90 95	
	ctt ggt ctc cgt aac ctc gat ctc ctc cta ggg tta gag aat cga gtc	336
	Leu Gly Leu Arg Asn Leu Asp Leu Leu Leu Gly Leu Glu Asn Arg Val	
	100 105 110	

	aat tac act tgc gtc gag gtt ata aac gga gat tgt cgt ctc gat caa	384
	Asn Tyr Thr Cys Val Glu Val Ile Asn Gly Asp Cys Arg Leu Asp Gln	
	115 120 125	
5	gct ctg gta cgt gat aag cgt tgg tcg aat ttc gaa ttg cta tgt ata	432
	Ala Leu Val Arg Asp Lys Arg Trp Ser Asn Phe Glu Leu Leu Cys Ile	
	130 135 140	
	tct aaa cct aga tcg aaa ctt ccg atg gga ttt ggt ggt aaa gca ttg	480
	Ser Lys Pro Arg Ser Lys Leu Pro Met Gly Phe Gly Gly Lys Ala Leu	
	145 150 155 160	
10	gaa tgg ctt gtg gat gcg ttg aaa act aga ccg gaa ggt tca ccg gat	528
	Glu Trp Leu Val Asp Ala Leu Lys Thr Arg Pro Glu Gly Ser Pro Asp	
	165 170 175	
	ttc atc atc atc gat tgt cct gca gga atc gat gcc gga ttc ata acc	576
	Phe Ile Ile Ile Asp Cys Pro Ala Gly Ile Asp Ala Gly Phe Ile Thr	
15	180 185 190	
	gcc att act ccg gcg aat gaa gca gtt ctg gta aca act ccg gat ata	624
	Ala Ile Thr Pro Ala Asn Glu Ala Val Leu Val Thr Thr Pro Asp Ile	
	195 200 205	
20	aca gcg tta agg gat gct gat agg gtt acg ggt ttg tta gaa tgc gat	672
	Thr Ala Leu Arg Asp Ala Asp Arg Val Thr Gly Leu Leu Glu Cys Asp	
	210 215 220	
	gga atc aga gat ata aag atg att gtg aac aga gtg aga act gat atg	720
	Gly Ile Arg Asp Ile Lys Met Ile Val Asn Arg Val Arg Thr Asp Met	
	225 230 235 240	
25	att aaa gga gag gat atg atg tca gtg tta gat gtg cag gag atg ttg	768
	Ile Lys Gly Glu Asp Met Met Ser Val Leu Asp Val Gln Glu Met Leu	
	245 250 255	
	gga ttg tca ttg ctt ggt gta att cct gaa gat tct gag gtt att cga	816
	Gly Leu Ser Leu Leu Gly Val Ile Pro Glu Asp Ser Glu Val Ile Arg	
30	260 265 270	
	agc acg aat cga ggg ttt ccg ctt gtt ctg aat aag cct cct acg ctt	864
	Ser Thr Asn Arg Gly Phe Pro Leu Val Leu Asn Lys Pro Pro Thr Leu	
	275 280 285	
35	gcg gga ttg gcg ttt gag cag gcg gct tgg aga ctc gtt gag caa gat	912
	Ala Gly Leu Ala Phe Glu Gln Ala Ala Trp Arg Leu Val Glu Gln Asp	
	290 295 300	
	agt atg aag gct gtt atg gtg gag gaa gaa cct aag aaa cgt ggc ttc	960
	Ser Met Lys Ala Val Met Val Glu Glu Glu Pro Lys Lys Arg Gly Phe	
	305 310 315 320	
40	ttc tct ttc ttt ggc ggc	978
	Phe Ser Phe Phe Gly Gly	
	325	

<210> 2  
 <211> 326  
 <212> PRT  
 <213> Arabidopsis thaliana

5 <400> 2

Met Ala Ser Leu Arg Leu Phe Ser Thr Asn His Gln Ser Leu Leu Leu  
 1 5 10 15

Pro Ser Ser Leu Ser Gln Lys Thr Leu Ile Ser Ser Pro Arg Phe Val  
 20 25 30

10 Asn Asn Pro Ser Arg Arg Ser Pro Ile Arg Ser Val Leu Gln Phe Asn  
 35 40 45

Arg Lys Pro Glu Leu Ala Gly Glu Thr Pro Arg Ile Val Val Ile Thr  
 50 55 60

15 Ser Gly Lys Gly Gly Val Gly Lys Thr Thr Thr Thr Ala Asn Val Gly  
 65 70 75 80

Leu Ser Leu Ala Arg Tyr Gly Phe Ser Val Val Ala Ile Asp Ala Asp  
 85 90 95

Leu Gly Leu Arg Asn Leu Asp Leu Leu Leu Gly Leu Glu Asn Arg Val  
 100 105 110

20 Asn Tyr Thr Cys Val Glu Val Ile Asn Gly Asp Cys Arg Leu Asp Gln  
 115 120 125

Ala Leu Val Arg Asp Lys Arg Trp Ser Asn Phe Glu Leu Leu Cys Ile  
 130 135 140

25 Ser Lys Pro Arg Ser Lys Leu Pro Met Gly Phe Gly Gly Lys Ala Leu  
 145 150 155 160

Glu Trp Leu Val Asp Ala Leu Lys Thr Arg Pro Glu Gly Ser Pro Asp  
 165 170 175

Phe Ile Ile Ile Asp Cys Pro Ala Gly Ile Asp Ala Gly Phe Ile Thr  
 180 185 190

30 Ala Ile Thr Pro Ala Asn Glu Ala Val Leu Val Thr Thr Pro Asp Ile  
 195 200 205

Thr Ala Leu Arg Asp Ala Asp Arg Val Thr Gly Leu Leu Glu Cys Asp  
 210 215 220

35 Gly Ile Arg Asp Ile Lys Met Ile Val Asn Arg Val Arg Thr Asp Met  
 225 230 235 240

Ile Lys Gly Glu Asp Met Met Ser Val Leu Asp Val Gln Glu Met Leu  
 245 250 255

Gly Leu Ser Leu Leu Gly Val Ile Pro Glu Asp Ser Glu Val Ile Arg  
 260 265 270

Ser Thr Asn Arg Gly Phe Pro Leu Val Leu Asn Lys Pro Pro Thr Leu  
275 280 285

Ala Gly Leu Ala Phe Glu Gln Ala Ala Trp Arg Leu Val Glu Gln Asp  
290 295 300

5 Ser Met Lys Ala Val Met Val Glu Glu Glu Pro Lys Lys Arg Gly Phe  
305 310 315 320

Phe Ser Phe Phe Gly Gly  
325

10 <210> 3  
<211> 1182  
<212> DNA  
<213> Tagetes erecta

<220>  
<221> CDS  
15 <222> (50) .. (934)

<400> 3  
aagcttgata tcgcaactcc ataactgatc ttctttcttct tctccggcg atg aca tcc 58  
Met Thr Ser  
1

20 ctg agg ttt cta aca gaa ccc tca ctt gta tgc tca tcc act ttc ccc 106  
Leu Arg Phe Leu Thr Glu Pro Ser Leu Val Cys Ser Ser Thr Phe Pro  
5 10 15

aca ttc aat ccc cta cac aaa acc cta act aaa cca aca cca aaa ccc 154  
Thr Phe Asn Pro Leu His Lys Thr Leu Thr Lys Pro Thr Pro Lys Pro  
25 20 25 30 35

tac cca aag cca cca cca att cgc tcc gtc ctt caa tac aat cgc aaa 202  
Tyr Pro Lys Pro Pro Ile Arg Ser Val Leu Gln Tyr Asn Arg Lys  
40 45 50

cca gag ctc gcc gga gac act cca cga gtc gtc gca atc gac gcc gac 250  
Pro Glu Leu Ala Gly Asp Thr Pro Arg Val Val Ala Ile Asp Ala Asp  
55 60 65

gtt ggt cta cgt aac ctc gat ctt ctt ctc ggt ctc gaa aac cgc gtc 298  
Val Gly Leu Arg Asn Leu Asp Leu Leu Leu Gly Leu Glu Asn Arg Val  
70 75 80

35 aat tac acc gtc gtt gaa gtt ctc aac ggc gat tgc aga ctc gac caa 346  
Asn Tyr Thr Val Val Glu Val Leu Asn Gly Asp Cys Arg Leu Asp Gln  
85 90 95

gcc cta gtt cgt gat aaa cgc tgg tca aat ttc gaa ttg ctt tgt att 394  
Ala Leu Val Arg Asp Lys Arg Trp Ser Asn Phe Glu Leu Leu Cys Ile  
40 100 105 110 115

tca aaa cct agg tca aaa ttg cct tta gga ttt ggg gga aaa gct tta 442  
Ser Lys Pro Arg Ser Lys Leu Pro Leu Gly Phe Gly Gly Lys Ala Leu  
120 125 130

gtt tgg ctt gat gca tta aaa gat agg caa gaa ggt tgc ccg gat ttt 490  
 Val Trp Leu Asp Ala Leu Lys Asp Arg Gln Glu Gly Cys Pro Asp Phe  
 135 140 145

5 ata ctt ata gat tgt cct gca ggt att gat gcc ggg ttc ata acc gcc 538  
 Ile Leu Ile Asp Cys Pro Ala Gly Ile Asp Ala Gly Phe Ile Thr Ala  
 150 155 160

att aca ccg gct aac gaa gcc gta tta gtt aca aca cct gat att act 586  
 Ile Thr Pro Ala Asn Glu Ala Val Leu Val Thr Thr Pro Asp Ile Thr  
 165 170 175

10 gca ttg aga gat gca gat aga gtt aca ggc ttg ctt gaa tgt gat gga 634  
 Ala Leu Arg Asp Ala Asp Arg Val Thr Gly Leu Leu Glu Cys Asp Gly  
 180 185 190 195

15 att agg gat att aaa atg att gtg aac aga gtt aga act gat ttg ata 682  
 Ile Arg Asp Ile Lys Met Ile Val Asn Arg Val Arg Thr Asp Leu Ile  
 200 205 210

agg ggt gaa gat atg atg tca gtt ctt gat gtt caa gag atg ttg gga 730  
 Arg Gly Glu Asp Met Met Ser Val Leu Asp Val Gln Glu Met Leu Gly  
 215 220 225

20 ttg tca ttg ttg agt gat acc cga gga ttc gaa gtg att cgg agt acg 778  
 Leu Ser Leu Leu Ser Asp Thr Arg Gly Phe Glu Val Ile Arg Ser Thr  
 230 235 240

aat aga ggg ttt ccg ctt gtg ttg aac aag cct ccg act tta gca gga 826  
 Asn Arg Gly Phe Pro Leu Val Leu Asn Lys Pro Pro Thr Leu Ala Gly  
 245 250 255

25 ttg gca ttt gag cag gct gct tgg aga ttg gtt gag caa gat agc atg 874  
 Leu Ala Phe Glu Gln Ala Ala Trp Arg Leu Val Glu Gln Asp Ser Met  
 260 265 270 275

30 aag gct gtg atg gtg gag gaa gaa cct aaa aag agg gga ttt ttc tcg 922  
 Lys Ala Val Met Val Glu Glu Glu Pro Lys Lys Arg Gly Phe Phe Ser  
 280 285 290

ttt ttt gga ggt tagtgatcga attcgttgaa tcgttgagtt gggtttgttt 974  
 Phe Phe Gly Gly  
 295

tgggtggagaa atgtgtcttg tttgttcattg taggagctgc tatgtgtcac ttgaaatggt 1034

35 atgtgtacag taagctgata aggattgttt taattcagtt ttcagagaga aaattagaat 1094

tgtagcaact tttcatttga tcaattcaat tgtatttctt tggttcagtg atgaattttt 1154

actcaaaatc aaaaaaaaaa aaaaaaaaaa 1182

<210> 4  
 <211> 295  
 <212> PRT  
 <213> Tagetes erecta

5 <400> 4  
 Met Thr Ser Leu Arg Phe Leu Thr Glu Pro Ser Leu Val Cys Ser Ser  
 1 5 10 15  
 Thr Phe Pro Thr Phe Asn Pro Leu His Lys Thr Leu Thr Lys Pro Thr  
 20 25 30  
 10 Pro Lys Pro Tyr Pro Lys Pro Pro Pro Ile Arg Ser Val Leu Gln Tyr  
 35 40 45  
 Asn Arg Lys Pro Glu Leu Ala Gly Asp Thr Pro Arg Val Val Ala Ile  
 50 55 60  
 15 Asp Ala Asp Val Gly Leu Arg Asn Leu Asp Leu Leu Leu Gly Leu Glu  
 65 70 75 80  
 Asn Arg Val Asn Tyr Thr Val Val Glu Val Leu Asn Gly Asp Cys Arg  
 85 90 95  
 Leu Asp Gln Ala Leu Val Arg Asp Lys Arg Trp Ser Asn Phe Glu Leu  
 100 105 110  
 20 Leu Cys Ile Ser Lys Pro Arg Ser Lys Leu Pro Leu Gly Phe Gly Gly  
 115 120 125  
 Lys Ala Leu Val Trp Leu Asp Ala Leu Lys Asp Arg Gln Glu Gly Cys  
 130 135 140  
 25 Pro Asp Phe Ile Leu Ile Asp Cys Pro Ala Gly Ile Asp Ala Gly Phe  
 145 150 155 160  
 Ile Thr Ala Ile Thr Pro Ala Asn Glu Ala Val Leu Val Thr Thr Pro  
 165 170 175  
 Asp Ile Thr Ala Leu Arg Asp Ala Asp Arg Val Thr Gly Leu Leu Glu  
 180 185 190  
 30 Cys Asp Gly Ile Arg Asp Ile Lys Met Ile Val Asn Arg Val Arg Thr  
 195 200 205  
 Asp Leu Ile Arg Gly Glu Asp Met Met Ser Val Leu Asp Val Gln Glu  
 210 215 220  
 35 Met Leu Gly Leu Ser Leu Leu Ser Asp Thr Arg Gly Phe Glu Val Ile  
 225 230 235 240  
 Arg Ser Thr Asn Arg Gly Phe Pro Leu Val Leu Asn Lys Pro Pro Thr  
 245 250 255  
 Leu Ala Gly Leu Ala Phe Glu Gln Ala Ala Trp Arg Leu Val Glu Gln  
 260 265 270

Asp Ser Met Lys Ala Val Met Val Glu Glu Glu Pro Lys Lys Arg Gly  
275 280 285

Phe Phe Ser Phe Phe Gly Gly  
290 295